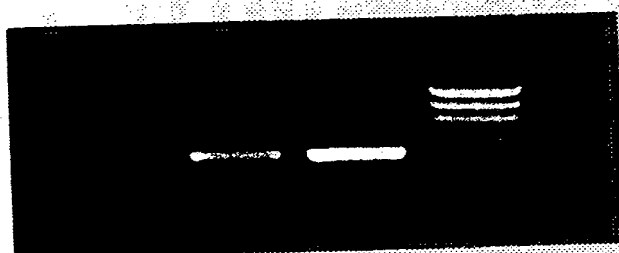
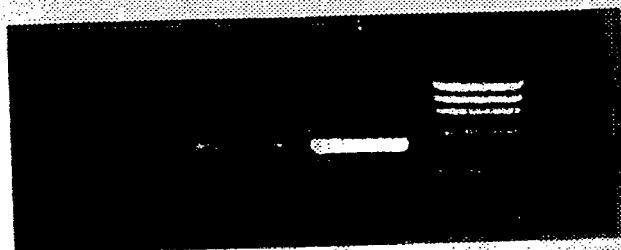


1/18

Control
Tumor I
Tumor II
Marker



PEX



GAPDH

FIG. 1

09806110-093404

TCTE 80-01193850

1 GAT CCA CTA GTA ACG GCC GCC AGT GTG GTG GAA TTC AAG GGA CTC ACA CAC TGA AAG AAT
 31
 61 TTT GAT GAA GAC AAT TCA GGC AAG CAG AAT GAT TCT TGC AAC AGA ATT ACA TGA TTA
 91
 ATC TTT GAT GAA GAC AAT TCA GGC AAG CAG AAT GAT TCT TGC AAC AGA ATT ACA TGA TTA
 151
 121 GAG ATC TTG AAG TGG GTC CGG TGA ATC CTG GCC ACC TAA CTT ATC ATG ATT TGG GGG
 211
 ATT GAG ATC TTG AAG TGG GTC CGG TGA ATC CTG GCC ACC TAA CTT ATC ATG ATT TGG GGG
 181
 181 TTC ACG AGA ATC CAG TTT TGA TAA AAC AAT TGT TTT CCT CCC CAA GTG ACT ATA
 271
 AGT TTC ACG AGA ATC CAG TTT TGA TAA AAC AAT TGT TTT CCT CCC CAA GTG ACT ATA
 241
 241 TTA AAT AGC TAA AAC ATC TGT TCA GCA ACA TAG TAA AAC ATA TAT ACT CGG AAC GCT
 331
 CAT TTA AAT AGC TAA AAC ATC TGT TCA GCA ACA TAG TAA AAC ATA TAT ACT CGG AAC GCT
 301
 301 GAG AAG AGC CTG CCA AAC AGG GAC TTT GCT GAG GGA GAG CAC CAA GAT AAA GCA ACA
 391
 TGA GAG AAG AGC CTG CCA AAC AGG GAC TTT GCT GAG GGA GAG CAC CAA GAT AAA GCA ACA
 361
 361 TTT GTT TTG TCT AGT CAG GGG GGA AAG CCA AGG CAA CCA ATA TTT TGG TTT TTA TAA
 451
 CTG TTT GTT TTG TCT AGT CAG GGG GGA AAG CCA AGG CAA CCA ATA TTT TGG TTT TTA TAA
 421
 421 TCA TTT GTG AAG AAT TAT TTG AGA AAG GGT TGG CGA GGG GAG ATT TCC TGA CGG CAG
 511
 TTT TCA TTT GTG AAG AAT TAT TTG AGA AAG GGT TGG CGA GGG GAG ATT TCC TGA CGG CAG
 481
 481 CTT AAG CTG TCC ATT AGT AGA AGA GCA AGA GAG CCT TGG ATG TCA ACG CCT CGC TCT
 571
 TTT CTT AAG CTG TCC ATT AGT AGA AGA GCA AGA GAG CCT TGG ATG TCA ACG CCT CGC TCT
 541
 541 GAC CAG CCA CCA AAC CAC GAA AAG TGA CTT TCT TCT CGT GTG CTC TCT ACG GCC CTT
 631/10
 TGA GAC CAG CCA CCA AAC CAC GAA AAG TGA CTT TCT TCT CGT GTG CTC TCT ACG GCC CTT
 601 /1
 601 /1 GAA GCA GAA ACA GGG AGC AGC GTG GAG ACT GGA AAG AAG GCC AAC AGA GGC ACT
 CTG ATG GAA GCA GAA ACA GGG AGC AGC GTG GAG ACT GGA AAG AAG GCC AAC AGA GGC ACT
 M E A E T G S S V E T G K K A N R G T
 691/30
 661/20
 CGA ATT GCC CTG GTC GTG TTT GTC GGT GGC ACC CTA GTT CTG GGC ACG ATC CTC TTT CTA
 R I A L V V F V G G T L V L G T I L F L
 2A (cont.)

TGTGGG GTTGGGG

721/40 GTG AGT CAA GGT CTC TTA AGT CTC CAA GCT AAA CAG GAG TAC TGC CTG AAG CCA GAA TGC
 V S Q G L L S L Q A K Q E Y C L K P E C
 781/60 ATC GAA GCG GCT GCT GCC ATC TTA AGT AAA GTA AAT CTG TCT GTG GAT CCT TGT GAT AAT
 I E A A A I L S K V N L S V D P C D N
 841/90 TTC TTC CGG TTC GCT TGT GAT GGC TGG ATA AGC AAT AAT CCA ATT CCC GAA GAT ATG CCA
 F F R F A C D G W I S N P I P E D M P
 901/100 AGC TAT GGG GTT TAT CCT TGG CTG AGA CAT AAT GTT GAC CTC AAG TTG AAG GAA CTT TTG
 S Y G V Y P W L R H N V D L K E L L
 961/120 GAG AAA TCA ATC AGT AGA AGG CGG GAC ACC GAA GCC ATA CAG AAA GCC AAA ATC CTT TAT
 E K S I S R R D T E A I Q K A K I L Y
 1021/140 TCA TCC TGC ATG AAT GAG AAA GCG ATT GAA AAA GCA GAT GCC AAG CCA CTG CTA CAC ATC
 S S C M N E K A I E K A D A K P L L H I
 1081/160 CTA CGG CAT TCA CCT TTC CGC TGG CCC GTG CTT GAA TCT AAT ATT GGC CCT GAA GGG GTT
 L R H S P F R W P V L E S N I G P E G V
 1141/180 TGG TCA GAG AGA AAG TTC AGC CTT CTG CAG ACA CTT GCA ACG TTT CGT GGT CAA TAC AGC
 W S E R K F S L L Q T L A T F R G Q Y S
 1201/200 AAT TCT GTG TTC ATC CGT TTG TAT GTG TCC CCT GAT GAC AAA GCA TCC AAT GAA CAT ATC
 N S V F I R L Y V S P D D K A S N E H I
 3/18 FIG - 2A (cont.)

TGTTCGCTTGTTCGCTT

1261/220
 TTG AAG CTG GAC CAA GCA ACA CTC TCC CTG GCC GTG AGG GAA GAC TAC CTT GAT AAC AGT
 L K L D Q A T L S L A V R E D Y L D N S
 1321/240
 ACA GAA GCC AAG TCT TAT CGG GAT GCC CTT TAC AAG TTC ATG GTG GAT ACT GCC GTG CTT
 T E A K S Y R D A L Y K F M V D T A V L
 1411/270
 1381/260
 TTA GGA GCT AAC AGT TCC AGA GCA GAG CAT GAC ATG AAG TCA GTG CTC AGA TTG GAA ATT
 L G A N S S R A E H D M K S V L R L E I
 1441/280
 AAG ATA GCT GAG ATA ATG ATT CCA CAT GAA AAC CGA ACC AGC GAG GCC ATG TAC AAC AAA
 K I A E I M I P H E N R T S E A M Y N K
 1501/300
 ATG AAC ATT TCT GAA CTG AGT GCT ATG ATT CCC CAG TTC GAC TGG CTG GGC TAC ATC AAG
 M N I S E L S A M I P Q F D W L G Y I K
 1561/320
 AAG GTC ATT GAC ACC AGA CTC TAC CCC CAT CTG AAA GAC ATC AGC CCC TCC GAG AAT GTG
 K V I D T R L Y P H L K D I S P S E N V
 1621/340
 GTG GTC CGC GTC CCG CAG TAC TTT AAA GAT TTG TTT AGG ATA TTA GGG TCT GAG AGA AAG
 V V R V P Q Y F K D L F R I L G S E R K
 1681/360
 AAG ACC ATT GCC AAC TAT TTG GTG TGG AGA ATG GTT TAT TCC AGA ATT CCA AAC CTT AGC
 K T I A N Y L V W R M V Y S R I P N L S
 1741/380
 AGG CGC TTT CAG TAT AGA TGG CTG GAA TTC TCA AGG GTA ATC CAG GGG ACC ACA ACT TTG
 R R F Q Y R W L E F S R V I Q G T T' T L
 4/18
 1591/330
 1651/350
 1711/370
 1771/390

TGTTCGCTTGTTCGCTT

- 2A (cont.)

PCT/CA99/00895

1801/400 1831/410
CTG CCT CAA TGG GAC AAA TGT GTA AAC TTT ATT GAA AGT GCC CTC CCT TAT GTT GTT GGA
L P Q W D K C V N F I E S A L P Y V V G

1861/420 1891/430
AAG ATG TTT GTA GAT GTG TAC TTC CAG GAA GAT AAG AAG GAA ATG ATG GAG GAA TTG GTT
K M F V D V Y F Q E D K K E M M E E L V

1921/440 1951/450
GAG GGC GTT CGC TGG GCC TTT ATT GAC ATG CTA GAG AAA GAA AAT GAG TGG ATG GAT GCA
E G V R W A F I D M L E K E N E W M D A

1981/460 2011/470
GGA ACG AAA AGG AAA GCC AAA GAA AAG GCG AGA GCT GTT TTG GCA AAA GCT GGC TAT CCA
G T K R K A K E K A R A V L A K V G Y P

2041/480 2071/490
GAG TTT ATA ATG AAT AAT N D T H V N E D L K A I K F S E
E F I M

2101/500 2131/510
GCC GAC TAC TTT GGC AAC GTC CTA CAA ACT CGC AAG TAT TTA GCA CAG TCT GAT TTC TTC
A D Y F G N V L Q T R K Y L A Q S D F F

2161/520 2191/530
TGG CTA AGA AAA GCC GTT CCA AAA ACA GAG TGG TTT ACA AAT CCG ACG ACT GTC AAT GCC
W L R K A V P K T E W F T N P T T V N A

2221/540 2251/550
TTC TAC AGT GCA TCC ACC AAC CAG ATC CGA TTT CCA GCA GAG GAG CTC CAG AAG CCT TTC
F Y S A S T N Q I R F P A G E L Q K P F

2281/560 2311/570
TTT TGG GGA ACA GAA TAT CCT CGA TCT CTG AGT TAT GGT GCT ATA GGA GTA ATT GTC GGA
F W G G T E Y P R S L S Y G A I G V I V G

- 2A (cont.)

TCTE 00-01190860

2341/580 2371/590
 CAT GAA TTT ACA CAT GGA TTT GAT AAT AAT GGT AGA AAA TAT GAT AAA AAT GGA AAC CTG
 H E F T H G F D N N G R K Y D K N G N L
 2401/600 2431/610
 GAT CCT TGG TGG TCT ACT GAA TCA GAA GAA AAG TTT AAG GAA AAA ACA AAA TGC ATG ATT
 D P W W S T E S E E K F K E K T K C M I
 2461/620 2491/630
 AAC CAG TAT AGC AAC TAT TAT TGG AAG AAA GCT GGC TTA AAT GTC AAG GGG AAG AGG ACC
 N Q Y S N Y Y W K K A G L N V K G K R T
 2521/640 2551/650
 CTG GGA GAA AAT ATT GCT GAT AAT GGA GGC CTG CGG GAA GCT TTT AGG GCT TAC AGG AAA
 L G E N I A D N G G L R E A F R A Y R K
 2581/660 2611/670
 TGG ATA AAT GAC AGA AGG CAG GGA CTT GAG GAG CCT CTT CTA CCA GGC ATC ACA TTC ACC
 W I N D R R Q G L E E P L L P G I T F T
 2641/680 2671/690
 AAC AAC CAG CTC TTC CTC AGT TAT GCT CAT GTG AGG TGC AAT TCC TAC AGA CCA GAA
 N N Q L F F L S Y A H V R C N S Y R P E
 2701/700 2731/710
 GCT GCC CGA GAA CAA GTC CAA ATT GGT GCT CAC AGT CCC CCT CAG TTT AGG GTC AAT GGT
 A A R E Q V Q I G A H S P P Q F R V N G
 2761/720 2791/730
 GCA ATT AGT AAC TTT GAA GAA TTC CAG AAA GCT TTT AAC TGT CCA CCC AAT TCC ACG ATG
 A I S N F E E F Q K A F N C P P N S T M
 2821/740 2851
 AAC AGA GGC ATG GAC TCC TGC CGA CTC TGG TAG CTG GGA CGC TGG TTT ATG GCA TCC TGA
 N R G M D S C R L W @

TCTE 00-01190860
 2A (cont.)

22881	GAC AGT TGC ACA GTG CCA GCG GAG GCT GCA	2991	CTG AGC CTT CAT CGC CCA TTG CTT TAG GCC
2941	TGG AGG AGC TTT CAT TTT TAG TGC ATT TTC	2971	ATT ATT TGG GTA GGT GAC CTG CTT GGA TCT
3001	AGA CAG CAT CTG TTC AAA GTT GTA GGG CTT	3031	ATA AAG TGG AAT ATA AGA AGA ACT AAG TAT
3051	GTT TCT TTA GAA AAT CAA ACC AAC AAA AAT	3091	AAA TCC CTA GGC TAC TTT TGT TAA AAA AAA
3121	AAA AAA AAA A		

 $\overline{\exists A} - \exists A$ (cont.)

8/18

T04E80-01190860

hPEX	10	20	30	40	50	60
	EAETGSSVETGKKANRGTRIALVVFVGTLVLGTILFLVSQGLLSLQAKQYCLKPECIE					
	:.....	:.....	:.....	:.....	:.....	:.....
hNEP	10	20	30	40	50	60
	ESQMDITDINTPKPKKKQRTWTPLEISLSVLVLLTIIAVTMIALYATYDDGICKSSDCIK					
	:.....	:.....	:.....	:.....	:.....	:.....
hPEX	70	80	90	100	110	120
	AAAAILSKVNSVDPDPCDNFFRFACDGIWISNNPIPEDMPSYGVYPLRHNVDLKLKELLEK					
	:.....	:.....	:.....	:.....	:.....	:.....
hNEP	70	80	90	100	110	120
	SAARLIQNMDATTEPCTDFFKYACGGWLKRNVIPETSSRYGNFDILRDELEVVLKDVLOE					
	:.....	:.....	:.....	:.....	:.....	:.....
hPEX	130	140	150	160	170	180
	SISRRRDTEAIIQAKILYSSCMNEKAIKADAKPILLHILRHSPFRWPVLESNIGPEGVWS					
	:.....	:.....	:.....	:.....	:.....	:.....
hNEP	130	140	150	160	170	180
	PKT--EDIVAVQKAKALYRSCINESAIDSRGGEPLKLLPDI-YGWPVATENWEQKYGAS					
	:.....	:.....	:.....	:.....	:.....	:.....
hPEX	190	200	210	220	230	240
	ERKFSLLQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTE					
	:.....	:.....	:.....	:.....	:.....	:.....
hNEP	190	200	210	220	230	240
	W---TAEKAIQALNSKYGKKVLINLFVGTDDKNSVNHVIHIDQPRGLPSRDYECTGIY					
	:.....	:.....	:.....	:.....	:.....	:.....

(cont.)

9/18

PAGE 01 OF 90860

	250	260	270	280	290
hPEX	AKSYRDALY-KFMVDTAVLLGANSSRAEH-----DMKSVLRLEIKIAEIMIPHENRT-SEA				
	240	250	260	270	280
hNEP	KEACTAYVDFMISVARLIRQEERLPIDENQALEMNKVMELKEKEIANATAKPEDRNDPML				
	300	310	320	330	340
hPEX	MYNKMNISEL-SAMIPQFDWLGYIK-KVIDTRLYPHLKDISPSENVVRVPQYFKDLFRI				
	300	310	320	330	340
hNEP	LYNKMTLAQIQNNFSLEINGKPFWSLNFTEIMSTVNISITNEEDVVVYAPEYLTCLKPI				
	360	370	380	390	400
hPEX	LGSERKKTIANYLVRMVYSRIPNLSRRFQYRWLEFSRVIQTTLLPQWDKCVNFIESA				
	360	370	380	390	400
hNEP	LTKYSARDLQNLMSWRFIMDLVSSLSRPTYKESRNAFRKALYGTTSATATWRRRCANYVNGN				

~~FILE~~ - 2B (cont.)

10/18

TABLE 10190860

hPEX	420	430	440	450	460	470
	LPYVVGKMFVDVVFQEDKKEMMEELVEGVRWAFIDMLEKENENWMDAGTKRKAKKEKARAVL					
hNEP	420	430	440	450	460	470
	MENAVGRLYVEAAPAGESKHVEDLIAQIREVFIQTLD-DLTWMDAETKKRAEEKALAIAK					
hPEX	480	490	500	510	520	530
	AKVGYPEFIM-NDTHVNEDLKAIFSEADYFGNVLQTRKYLAQSDFFWLKAVPKTEWFT					
hNEP	480	490	500	510	520	530
	ERIGYPDDIVSNDNKLNNLEYLELNYKEDEYFENIIQNLKFSQSKQLKKLREKVDKDEWIS					
hPEX	540	550	560	570	580	590
	NPTTVNAFYASTNQIRFPAGELQKPPFFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRK					
hNEP	540	550	560	570	580	590
	GAAVVNAFYSSGRNQIVFPAGILQPPFFSAQQSN-SLNYGGIGMVGIEITHGFDNNGRN					

TABLE 10190860 (cont.)

11/18

PCT/CA99/00895

hPEX	600	610	620	630	640	650
	YDKNGNLDPW	STEESEKFK	EKTKCMINQ	YSNYWKAG	-LNVKGR	TLGENIADNGGLR

hNEP	600	610	620	630	640	650
	FNKDGDLVD	WWTQQSAS	NFKESQCM	VYQYGNF	SWDLAGGQ	HNLGINTLGENIADNGGLG

hPEX	660	670	680	690	700	710
	EAFRAYRKW	INDRRQGLE	EPLPGIT	TFTNNQL	FFLSYAHV	RCNSYRPEAAREQVQIGAHS

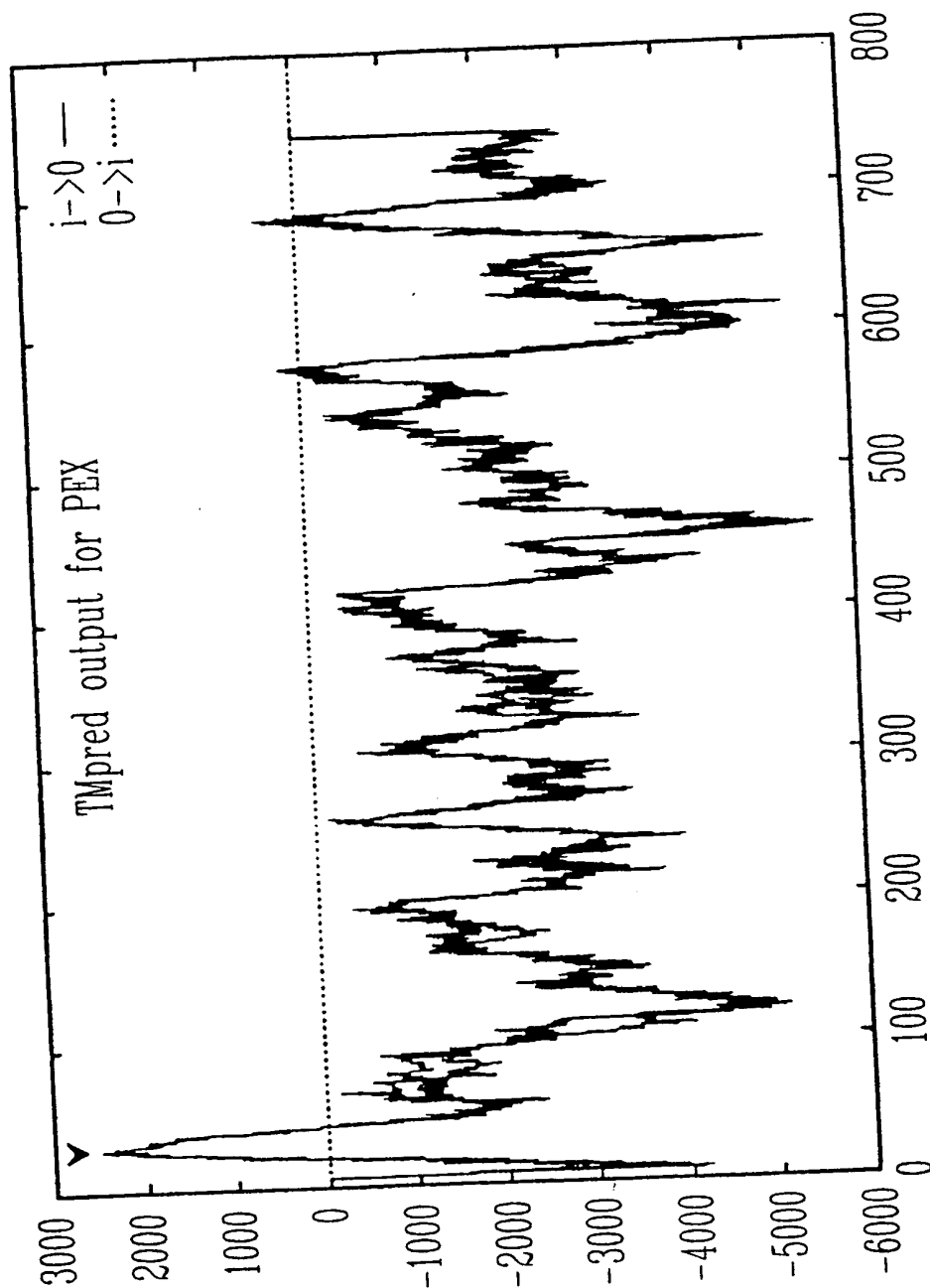
hNEP	660	670	680	690	700	710
	QAYRAYQ---	NYIKKNGE	EKLLPGLD	LNHKQL	FFLNFAQV	WCGTYRPEYAVNSIKTDVHS

hPEX	720	730	740			
	PPQFRVNGA	ISNFEEFQ	KAFCPPN	STMNRGMD	SCRLW	
	
hNEP	720	730	740	750		
	PGNFRIIGT	LQNSAEF	SEAFHCR	KNSYMNPE	KK-CRVW	
	

~~718~~ - 28 (cont.)

12/18

PAGE 01 OF 01

FIG. 2C

13/18

Saos-2
Tumor 1

28 S
18 S

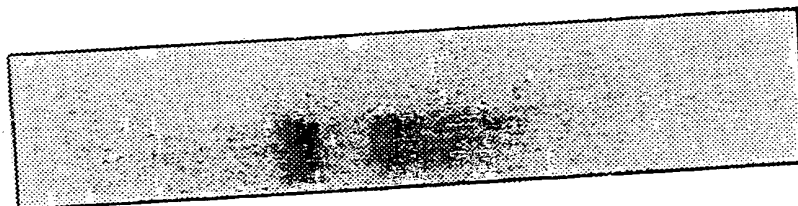


Fig. 4

Marker
Control
Tumor 1
Adult kidney
Fetal muscle
Fetal kidney
Fetal calvaria
Saos-2

PEX

Relative Expression

100
50

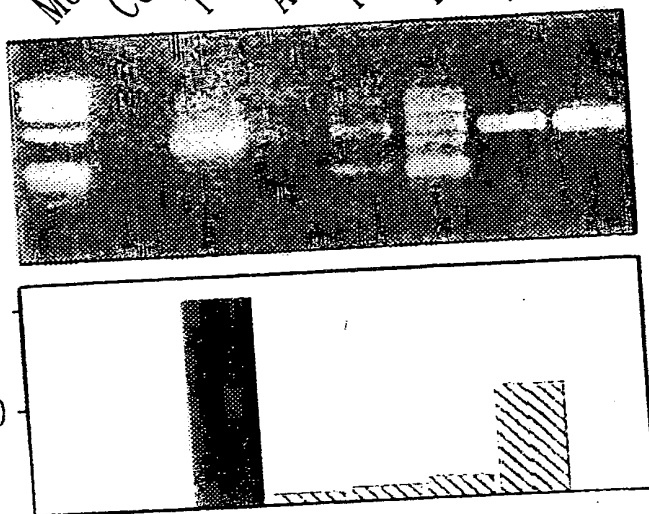
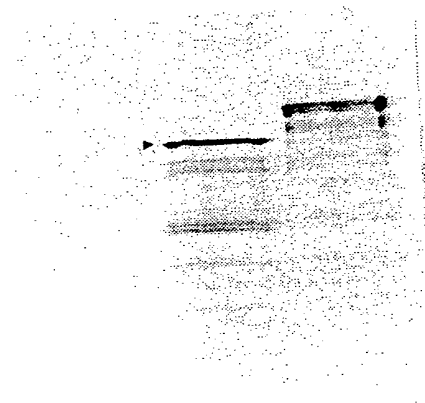


Fig. 5

14/18

09806110.083104

mRNA	-	+	+
Membranes	-	-	+



Mr (10³)

◀ 97.1

◀ 66.4

◀ 42.7

Fig. 5

15/18
TX114

A

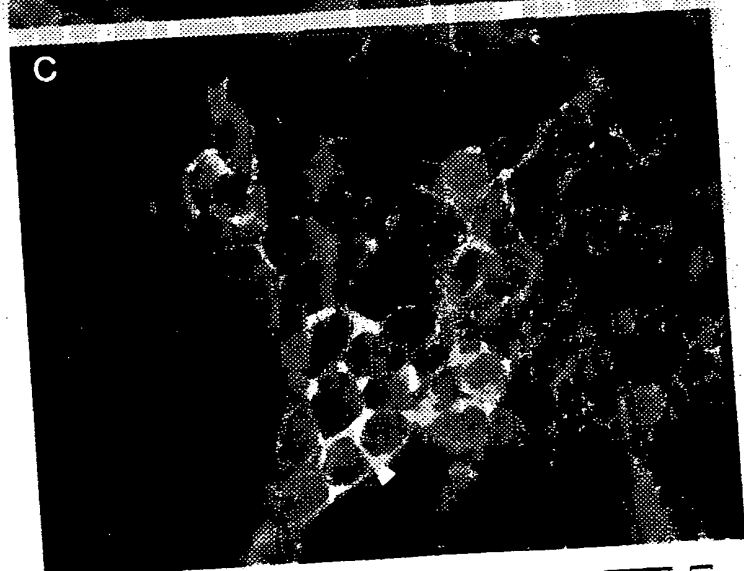
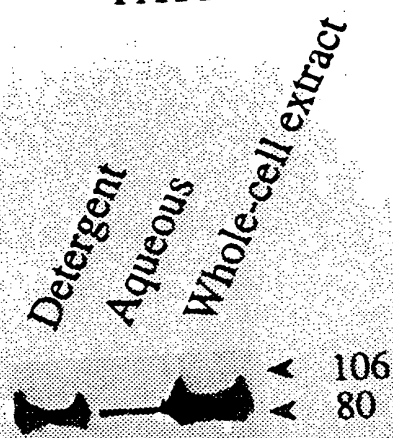
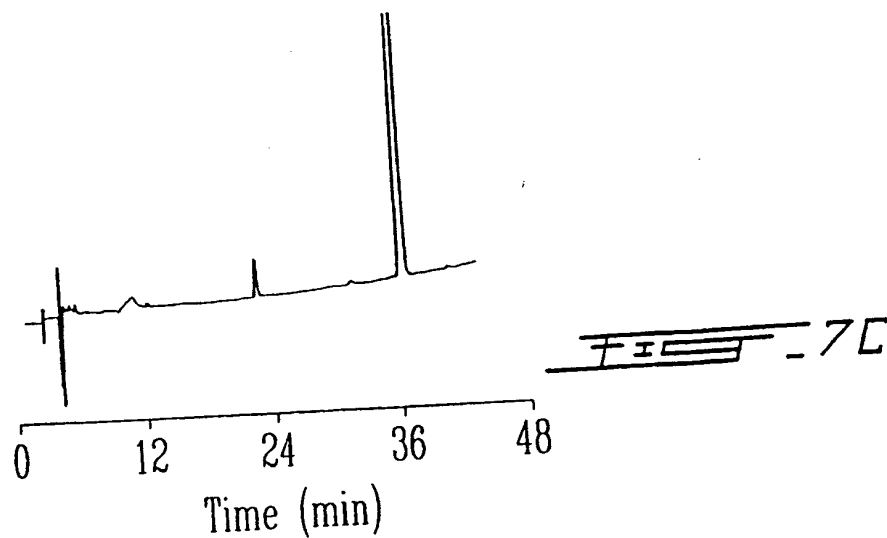
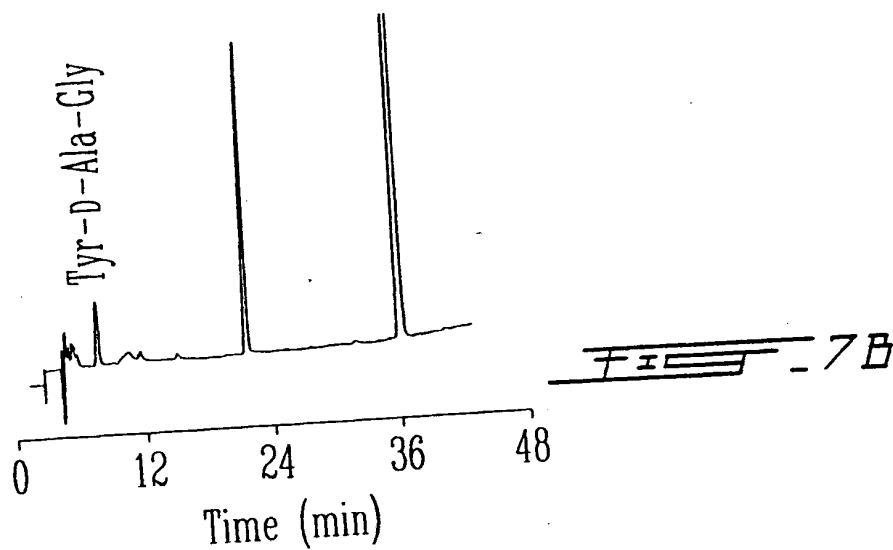
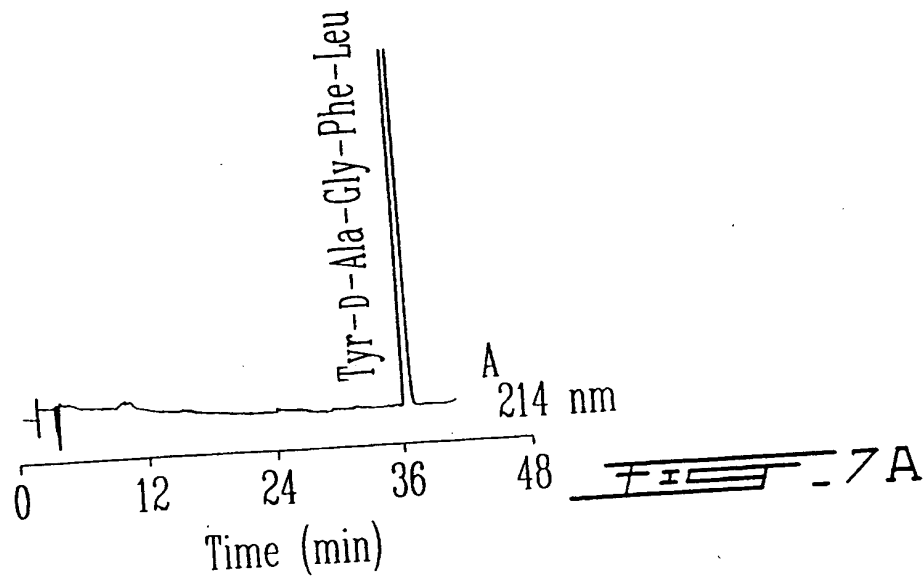
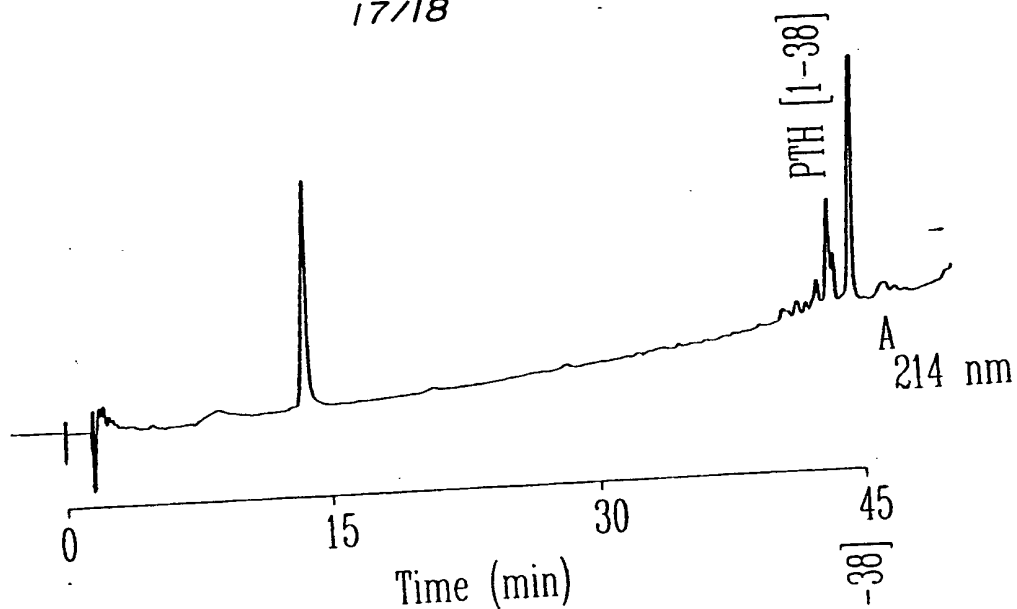


FIG. 6

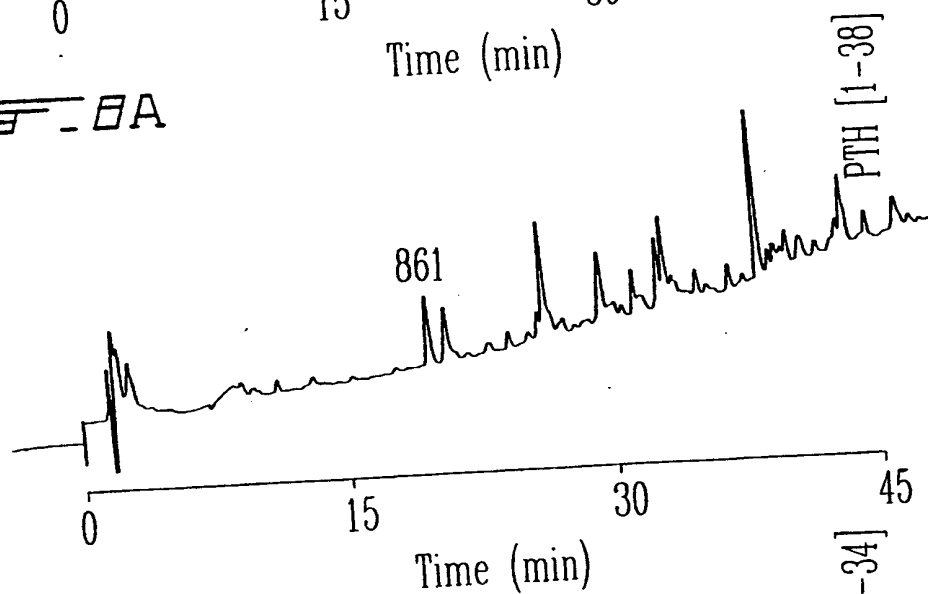
16/18



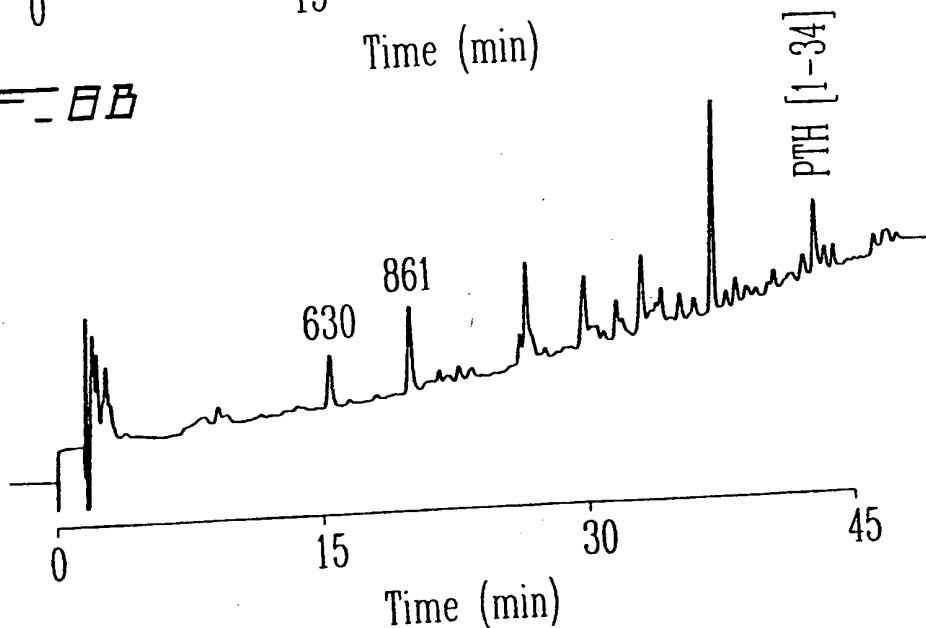
17/18



FIIS - BA



FIIS - BB



FIIS - BC

18/18

FIG. 18

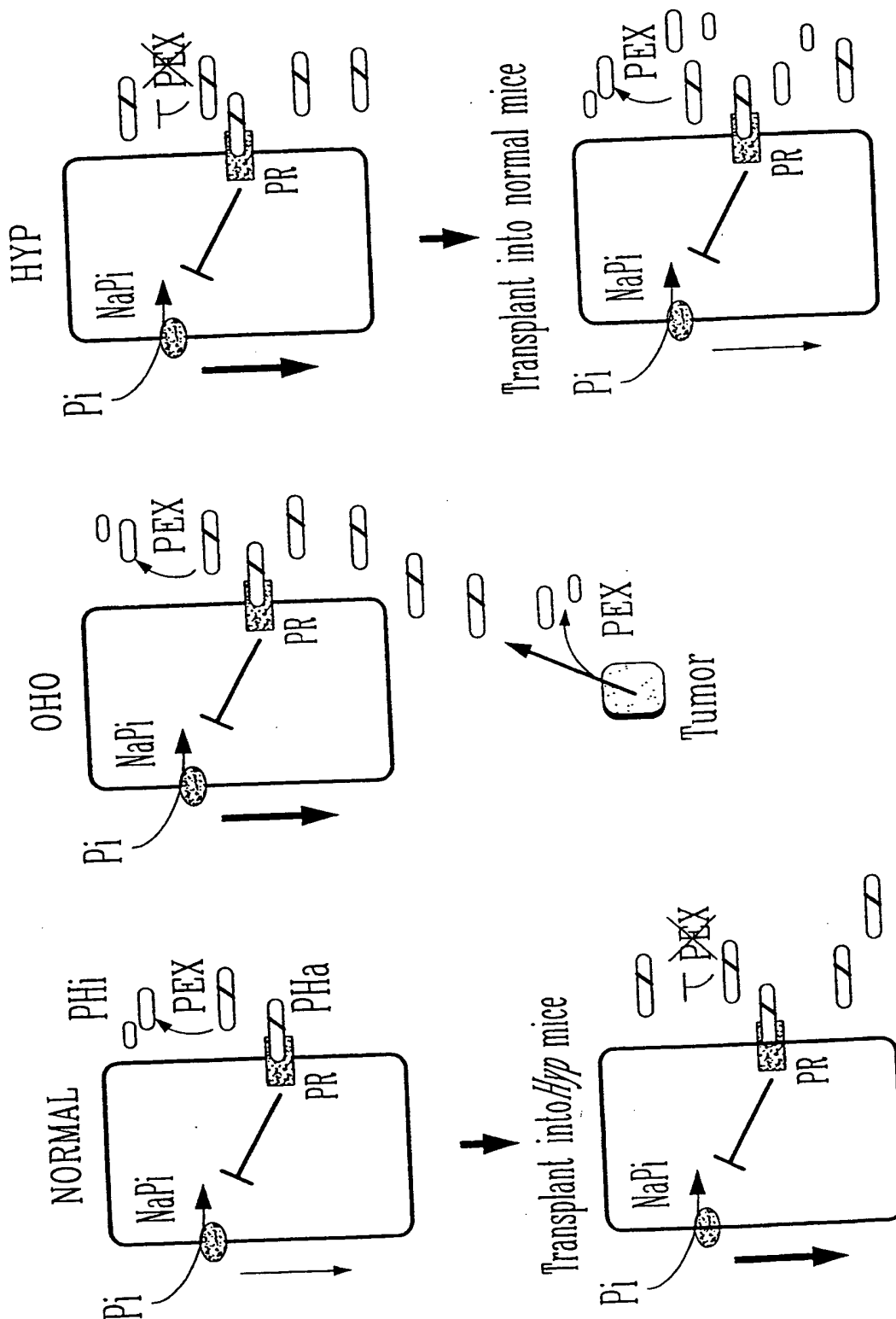


FIG. 18